

SEQUENCE LISTING

<110> Salkoff, Lawrence
Schreiber, Matthew
Silvia, Chris
The Washington University
ICAgene Inc.

<120> A pH Sensitive Potassium Channel in Spermatocytes

<130> 018512-000120US

<140> 09/176,664

<141> 1998-10-21

<150> US 60/063,138

<151> 1997-10-22

<150> US 60/076,172

<151> 1998-02-27

<160> 53

<170> PatentIn Ver. 2.0

<210> 1

<211> 1112

<212> PRT

<213> Mus musculus

<220>

<223> mouse Slo3 (mSlo3)

<220>

<221> VARIANT

<222> (5)

<223> polymorphic variant #2 Leu -> Ile

<220>

<221> VARIANT

<222> (21)

<223> polymorphic variant #1 Ile -> Val

<220>

<221> VARIANT

<222> (25)

<223> polymorphic variant #3 Ala -> Ser

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Met Ser Gln Thr Leu Leu Asp Ser Leu Asn Gln Lys Glu Leu Thr Glu
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Thr Ser Cys Thr Ile Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Leu
20 25 30

Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala
35 40 45

Leu Lys Ser Ser Arg Ser Trp Lys Tyr Val Lys Gly Pro Arg Gly Leu
50 55 60

Leu 65	Glu	Leu	Phe	Ser	Ser 70	Arg	Arg	Ile	Glu	Ala 75	Asn	Pro	Leu	Arg	Lys 80
Leu	Tyr	Phe	His	Gly 85	Val	Phe	Arg	Gln	Arg 90	Ile	Glu	Met	Leu	Leu	Ser 95
Ala	Gln	Thr	Val 100	Val	Gly	Gln	Val	Leu 105	Val	Ile	Leu	Val	Phe 110	Val	Leu
Ser	Ile	Gly 115	Ser	Leu	Val	Ile	Tyr 120	Phe	Ile	Asn	Ser	Met 125	Asp	Pro	Val
Arg	Arg 130	Cys	Ser	Ser	Tyr	Glu 135	Asp	Lys	Ile	Val	His 140	Gly	Asp	Leu	Ser
Phe 145	Asn	Ala	Phe	Phe	Ser 150	Phe	Tyr	Phe	Gly	Leu 155	Arg	Phe	Trp	Ala	Ala 160
Glu	Asp	Lys	Ile	Lys 165	Phe	Trp	Leu	Glu	Met 170	Asn	Ser	Ile	Val	Asp 175	Ile
Phe	Thr	Ile	Pro 180	Pro	Thr	Phe	Ile	Ser 185	Tyr	Tyr	Leu	Lys	Ser 190	Asn	Trp
Leu	Gly 195	Leu	Arg	Phe	Leu	Arg	Ala 200	Leu	Arg	Leu	Leu	Glu 205	Leu	Pro	Lys
Ile 210	Leu	Gln	Ile	Leu	Gln	Val 215	Ile	Lys	Thr	Ser	Asn 220	Ser	Val	Lys	Leu
Ser 225	Lys	Leu	Leu	Ser	Ile 230	Val	Ile	Ser	Thr	Trp 235	Phe	Thr	Ala	Ala	Gly 240
Phe	Leu	His	Leu	Val 245	Glu	Asn	Ser	Gly	Asp 250	Pro	Trp	Leu	Asn	Gly 255	Arg
Asn	Ser	Gln	Thr 260	Met	Ser	Tyr	Phe	Glu 265	Ser	Ile	Tyr	Leu	Val 270	Thr	Ala
Thr	Met	Ser 275	Thr	Val	Gly	Phe	Gly 280	Asp	Val	Val	Ala	Lys 285	Thr	Ser	Leu
Gly 290	Arg	Ile	Phe	Ile	Val	Phe 295	Phe	Thr	Leu	Gly	Ser 300	Leu	Ile	Leu	Phe
Ala 305	Asn	Tyr	Ile	Pro	Glu 310	Met	Val	Glu	Leu	Phe 315	Ser	Thr	Arg	Lys	Lys 320
Tyr	Thr	Lys	Pro 325	Tyr	Glu	Ala	Val	Lys	Gly 330	Lys	Lys	Phe	Ile	Val 335	Val
Cys	Gly	Asn	Ile 340	Thr	Val	Asp	Ser	Val 345	Thr	Ala	Phe	Leu	Arg 350	Asn	Phe
Leu	His	Trp 355	Lys	Ser	Gly	Glu 360	Ile	Asn	Ile	Glu	Ile	Val 365	Phe	Leu	Gly
Glu 370	Thr	Leu	Pro	Cys	Leu	Glu 375	Leu	Glu	Thr	Leu	Leu 380	Lys	Cys	His	Thr

Ser 385	Cys	Thr	Asn	Phe	Val 390	Cys	Gly	Thr	Ala	Leu 395	Lys	Phe	Glu	Asp	Leu 400
Lys	Arg	Val	Ala	Val 405	Glu	Asn	Ser	Glu	Ala 410	Cys	Leu	Ile	Leu	Ala	Asn 415
His	Phe	Cys	Ser	Asp 420	Leu	His	Asp	Glu 425	Asp	Asn	Ser	Asn	Ile	Met	Arg 430
Val	Leu	Ser	Ile	Lys	Asn	Tyr	Tyr 440	Pro	Gln	Thr	Arg	Val 445	Ile	Ile	Gln
Ile	Leu	Gln	Ser	Gln	Asn	Lys 455	Val	Phe	Leu	Ser	Lys 460	Ile	Pro	Asn	Trp
Asp 465	Trp	Ser	Ala	Gly	Asp 470	Asn	Ile	Leu	Cys	Phe 475	Ala	Glu	Leu	Lys	Leu 480
Gly	Phe	Ile	Ala	Gln 485	Gly	Cys	Leu	Val 490	Pro	Gly	Leu	Cys	Thr	Phe	Leu 495
Thr	Thr	Leu	Phe 500	Ile	Glu	Gln	Asn 505	Gln	Lys	Val	Phe	Pro	Lys 510	His	Pro
Trp	Gln	Lys 515	His	Phe	Leu	Asn	Gly 520	Leu	Lys	Asn	Lys	Ile 525	Leu	Thr	Gln
Arg	Leu 530	Ser	Asn	Asp	Phe	Val 535	Gly	Met	Thr	Phe 540	Pro	Gln	Val	Ser	Arg
Leu 545	Cys	Phe	Val	Lys	Leu 550	Asn	Leu	Met	Leu	Ile 555	Ala	Ile	Gln	His	Lys 560
Pro	Phe	Phe	His	Ser 565	Cys	Cys	Thr	Leu	Ile 570	Leu	Asn	Pro	Ser	Ser 575	Gln
Val	Arg	Leu	Asn 580	Lys	Asp	Thr	Leu	Gly 585	Phe	Phe	Ile	Ala	Asp 590	Ser	Ser
Lys	Ala	Val 595	Lys	Arg	Ala	Phe	Phe 600	Tyr	Cys	Ser	Asn	Cys 605	His	Ser	Asp
Val	Cys 610	Asn	Pro	Glu	Leu	Ile 615	Gly	Lys	Cys	Asn	Cys 620	Lys	Ile	Lys	Ser
Arg 625	Gln	Gln	Leu	Ile	Ala 630	Pro	Thr	Ile	Met	Val 635	Met	Lys	Ser	Ser	Leu 640
Thr	Asp	Phe	Thr	Thr 645	Ser	Ser	His	Ile	His 650	Ala	Ser	Met	Ser	Thr	Glu 655
Ile	His	Thr	Cys 660	Phe	Ser	Arg	Glu	Gln 665	Pro	Ser	Leu	Ile	Thr 670	Ile	Thr
Thr	Asn	Arg 675	Pro	Thr	Thr	Asn	Asp 680	Thr	Val	Asp	Asp	Thr 685	Asp	Met	Leu
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05015076 000000

Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His
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Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu
725 730 735

Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu
740 745 750

Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu
755 760 765

Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser
770 775 780

Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser
785 790 795 800

Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
805 810 815

Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Asn Ile Gln Ser Leu
820 825 830

Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro
835 840 845

Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile
850 855 860

Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu
865 870 875 880

Gln Met Gly Gly Leu Asp Gly Met Leu Lys Gly Thr Ser Leu His Leu
885 890 895

Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp
900 905 910

Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu
915 920 925

Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu
930 935 940

Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys
945 950 955 960

Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr
965 970 975

Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys
980 985 990

Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met
995 1000 1005

Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr
1010 1015 1020

Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
1025 1030 1035 1040

Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
1045 1050 1055

Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg Arg His Trp Pro
1060 1065 1070

Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile
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1090 1095 1100

Pro Glu Ser Ile Leu Trp Thr Arg
1105 1110

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<213> Mus musculus

<220>
<223> mouse Slo3 (mSlo3)

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atcttattcc ttttcagaat agccttgaaa agctcaagaa gttggaaata cgtcaagggg 180
ccaagaggac tcttggaact attctcatca cgtagaatcg aggctaattcc tttgaggaaa 240
ctttactttc atggagtatt tcgtcagcgc atcgaaatgc tgctttctgc acagaccgtc 300
gtggggcaag tgttggtgat ccttgtcttt gtactaagca tcgggtctct tgtgatctat 360
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ggggatttga gtttcaacgc tttcttttagc ttctattttg gggtgaggtt ttgggcagct 480
gaagacaaga tcaagttctg gttggagatg aattcaattg tagacatttt taccatcccg 540
ccaaccttta tttcttatta tttgaagagt aattggctag gtttgagatt tctaagagct 600
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tcagtgaagc ttcccaaact gttgtcaata gttatcagta cctgggtcac ggcagcagga 720
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ccacagacca gagtcatcat tcagatactt cagtctcaaa acaaggtttt cctgtcaaaa 1380
atccccaact gggactggag tgctggagac aatatcctct gctttgcaga gctaaagctc 1440
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ttgaagaaca agattctgac acagcgctc tctaacgact tcgtggggat gacatttccc 1620
caggtctccc ggctctgctt tgtgaagcta aatctcatgc tgatcgccat ccaacacaag 1680
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aaaatcaaga gccgacaaca actcatagca ccgaccatca tgggtgatgaa aagcagcttg 1920
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 <211> 416
 <212> DNA
 <213> Homo sapiens

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 <223> human Slo3 (hSlo3)

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 attatcttgg aactgttcac atcaggtacc atcgctagga gccatgtaag aagcctccac 180
 ttccagggac aatttcgtga tcatatagaa atgttgcttt cagcccagac ctttgtgggg 240
 caagtgttgg tgatccttgt ctttgtacta agcattgggt ctcttataat ctatttcac 300
 aattcwgctg accctgttgg aacgctgttc atcatatgaa gacaaaacca ttcctattga 360
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<210> 5
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 <212> PRT
 <213> Mus musculus

<220>
 <221> PEPTIDE
 <222> (1)..(4)
 <223> mSlo3 peptide starting with amino acid 687

<400> 5
 Met Leu Asp Ser
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<210> 6
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human Slo3-b (hSlo3-b)

<220>
 <221> MOD_RES
 <222> (29)
 <223> Xaa = any amino acid

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 Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile Leu Glu Leu Phe Thr Ser
 35 40 45
 Gly Thr Ile Ala Arg Ser His Val Arg Ser Leu His Phe Gln Gly Gln
 50 55 60
 Phe Arg Asp His Ile Glu Met Leu Leu Ser Ala Gln Thr Phe Val Gly
 65 70 75 80

009060"006060

THE FUTURE OF THE FUTURE

<223> Description of Artificial Sequence:mSlo3 primer

<400> 9

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28

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 primer

<400> 10

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22

<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:mSlo3 primer

<400> 11

tttcaaagcc tcttttagcgg taa

23

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 primer

<400> 12

ttatgcctgg atctgcactc tacatg

26

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 primer

<400> 13

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23

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

2025年12月25日

<223> Description of Artificial Sequence:hSlo3 primer

<400> 14

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24

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:hSlo3 primer

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<210> 16

<211> 1105

<212> PRT

<213> Homo sapiens

$\langle 220 \rangle$

<223> human Slo3-1 (hSlo3-1)

<220>

<221> VARIANT

<222> (6)

<223> polymorphic variant #2 Leu -> Ile

<220>

<221> VARIANT

<222> (23)

<223> polymorphic variant #1 Ile -> Val

<220>

<221> VARIANT

<222> (25)

<223> polymorphic variant #3 Ala -> Ser

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Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Leu Ile Phe Arg Leu Ile
35 40 45

Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
50 55 60

Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
65 70 75 80

Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
85 90 95

Pro	Leu	Cys	Ser	Asp	Ser	His	Ala	Glu	Asp	Ile	Ser	Asn	Ile	Met	Arg
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Val	Leu	Ser	Ile	Lys	Asn	Tyr	Asp	Ser	Thr	Thr	Arg	Ile	Ile	Ile	Gln
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Ile	Leu	Gln	Ser	His	Asn	Lys	Val	Tyr	Leu	Pro	Lys	Ile	Pro	Ser	Trp
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Asn	Trp	Asp	Thr	Gly	Asp	Asn	Ile	Ile	Cys	Phe	Ala	Glu	Leu	Lys	Leu
465					470					475					480
Gly	Phe	Ile	Ala	Gln	Gly	Cys	Leu	Val	Pro	Gly	Leu	Cys	Thr	Phe	Leu
				485					490					495	
Thr	Ser	Leu	Phe	Val	Glu	Gln	Asn	Lys	Lys	Val	Met	Pro	Lys	Gln	Thr
			500					505					510		
Trp	Lys	Lys	His	Phe	Leu	Asn	Ser	Met	Lys	Asn	Lys	Ile	Leu	Thr	Gln
		515					520					525			
Arg	Leu	Ser	Asp	Asp	Phe	Ala	Gly	Met	Ser	Phe	Pro	Glu	Val	Ala	Arg
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Leu	Cys	Phe	Leu	Lys	Met	Tyr	Leu	Leu	Leu	Ile	Ala	Ile	Glu	Tyr	Lys
545					550					555					560
Ser	Leu	Phe	Thr	Asp	Gly	Phe	Cys	Gly	Leu	Ile	Leu	Asn	Pro	Pro	Pro
				565					570					575	
Gln	Val	Arg	Ile	Arg	Lys	Asn	Thr	Leu	Gly	Phe	Phe	Ile	Ala	Glu	Thr
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Pro	Lys	Asp	Val	Arg	Arg	Ala	Leu	Phe	Tyr	Cys	Ser	Val	Cys	His	Asp
		595					600					605			
Asp	Val	Phe	Ile	Pro	Glu	Leu	Ile	Thr	Asn	Cys	Gly	Cys	Lys	Ser	Arg
	610					615					620				
Ser	Arg	Gln	His	Ile	Thr	Val	Pro	Ser	Val	Lys	Arg	Met	Lys	Lys	Cys
625					630					635					640
Leu	Lys	Gly	Ile	Ser	Ser	Arg	Ile	Ser	Gly	Gln	Asp	Ser	Pro	Pro	Arg
				645					650					655	
Val	Ser	Ala	Ser	Thr	Ser	Ser	Ile	Ser	Asn	Phe	Thr	Thr	Arg	Thr	Leu
			660					665					670		
Gln	His	Asp	Val	Glu	Gln	Asp	Ser	Asp	Gln	Leu	Asp	Ser	Ser	Gly	Met
		675					680					685			
Phe	His	Trp	Cys	Lys	Pro	Thr	Ser	Leu	Asp	Lys	Val	Thr	Leu	Lys	Arg
	690					695					700				
Thr	Gly	Lys	Ser	Lys	Tyr	Lys	Phe	Arg	Asn	His	Ile	Val	Ala	Cys	Val
705					710					715					720
Phe	Gly	Asp	Ala	His	Ser	Ala	Pro	Met	Gly	Leu	Arg	Asn	Phe	Val	Met
				725					730					735	

Pro Leu Arg Ala Ser Asn Tyr Thr Arg Lys Glu Leu Lys Asp Ile Val
 740 745 750
 Phe Ile Gly Ser Leu Asp Tyr Leu Gln Arg Glu Trp Arg Phe Leu Arg
 755 760 765
 Asn Phe Pro Gln Ile Tyr Ile Leu Pro Gly Cys Ala Leu Tyr Ser Gly
 770 775 780
 Asp Leu His Ala Ala Asn Ile Glu Gln Cys Ser Met Cys Ala Val Leu
 785 790 795 800
 Ser Pro Pro Pro Gln Pro Ser Ser Asn Gln Thr Leu Val Asp Thr Glu
 805 810 815
 Ala Ile Met Ala Thr Leu Thr Ile Gly Ser Leu Gln Ile Asp Ser Ser
 820 825 830
 Ser Asp Pro Ser Pro Ser Val Ser Glu Glu Thr Pro Gly Tyr Thr Asn
 835 840 845
 Gly His Asn Glu Lys Ser Asn Cys Arg Lys Val Pro Ile Leu Thr Glu
 850 855 860
 Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu Gln Leu Gly Gly Leu
 865 870 875 880
 Glu Gly Ser Leu Gln Glu Thr Asn Leu His Leu Ser Thr Ala Phe Ser
 885 890 895
 Thr Gly Thr Val Phe Ser Ser Ser Phe Leu Asp Ser Leu Leu Ala Thr
 900 905 910
 Ala Phe Tyr Asn Tyr His Val Leu Glu Leu Leu Gln Met Leu Val Thr
 915 920 925
 Gly Gly Val Ser Ser Gln Leu Glu Gln His Leu Asp Lys Asp Lys Val
 930 935 940
 Tyr Gly Val Ala Asp Ser Cys Thr Ser Leu Leu Ser Gly Arg Asn Arg
 945 950 955 960
 Cys Lys Leu Gly Leu Leu Ser Leu His Glu Thr Ile Leu Ser Asp Val
 965 970 975
 Asn Pro Arg Asn Thr Phe Gly Gln Leu Phe Cys Gly Ser Leu Asp Leu
 980 985 990
 Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Ile Ile Asp Glu Glu Glu
 995 1000 1005
 Leu Asn Pro Glu Asn Lys Arg Phe Val Ile Thr Arg Pro Ala Asn Glu
 1010 1015 1020
 Phe Lys Leu Leu Pro Ser Asp Leu Val Phe Cys Ala Ile Pro Phe Ser
 1025 1030 1035 1040
 Thr Ala Cys Tyr Lys Arg Asn Glu Glu Phe Ser Leu Gln Lys Ser Tyr
 1045 1050 1055

Glu Ile Val Asn Lys Ala Ser Gln Thr Thr Glu Asp Thr Phe Arg His
 1060 1065 1070

Lys Leu Ser Ser His Pro Leu Ile Gln Leu Leu Arg His Cys Ile His
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Gln Ser Ile Leu Thr Ser Arg Glu Leu Thr Pro Ser Leu Phe Leu Ser
 1090 1095 1100

Lys
 1105

<210> 17
 <211> 3319
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human Slo3-1 (hSlo3-1)

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 Arg Lys Val Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His
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 Phe Ile Glu Gln Leu Gly Gly Leu Glu Gly Ser Leu Gln Glu Thr Asn
 850 855 860
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 865 870 875 880
 Phe Leu Asp Ser Leu Leu Ala Thr Ala Phe Tyr Asn Tyr His Val Leu
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 <223> human Slo3-2 (hSlo3-2)


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Tyr	Thr	Lys	Pro	Tyr	Glu	Ala	Val	Lys	Gly	Lys	Lys	Phe	Ile	Val	Val
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Lys	Arg	Val	Ala	Val	Glu	Asn	Ser	Glu	Ala	Cys	Leu	Ile	Leu	Ala	Asn
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Gly	Phe	Ile	Ala	Gln	Gly	Cys	Leu	Val	Pro	Gly	Leu	Cys	Thr	Phe	Leu
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Lys	Ala	Val	Lys	Arg	Ala	Phe	Phe	Tyr	Cys	Ser	Asn	Cys	His	Ser	Asp
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Thr	Asp	Phe	Thr	Thr	Ser	Ser	His	Ile	His	Ala	Ser	Met	Ser	Thr	Glu
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Ile	His	Thr	Cys	Phe	Ser	Arg	Glu	Gln	Pro	Ser	Leu	Ile	Thr	Ile	Thr
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Asp	Ser	Ser	Gly	Met	Phe	His	Trp	Cys	Arg	Ala	Met	Pro	Leu	Asp	Lys
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Ile	Val	Val	Cys	Val	Phe	Gly	Asp	Ala	Gln	Cys	Thr	Leu	Val	Gly	Leu
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Trp	Arg	Phe	Leu	Arg	Asn	Phe	Pro	Lys	Ile	His	Ile	Met	Pro	Gly	Ser
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Ser	Ser	Ala	Phe	Asp	Ser	Lys	Glu	Arg	Lys	Gln	Arg	Tyr	Lys	Gln	Ile
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Pro	Asp	Ala	Glu	Asp	Ala	Ser	Asn	Ile	Met	Arg	Val	Ile	Ser	Ile	Lys	
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Ser	Cys	Leu	Ala	Gln	Gly	Leu	Ser	Thr	Met	Leu	Ala	Asn	Leu	Phe	Ser	
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625					630					635					640	
Pro	Pro	Thr	Leu	Ser	Pro	Lys	Lys	Lys	Gln	Arg	Asn	Gly	Gly	Met	Arg	
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		675					680					685				

Pro	Thr	Asp	Ser	Pro	Phe	Asp	Ala	Asp	Asp	Cys	Leu	Lys	Val	Arg	Lys
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Leu	Val	Val	Leu	Leu	Trp	Arg	Ala	Phe	Ala	Phe	Val	Ser	Cys	Arg	Lys
	65				70					75					80
Glu	Pro	Asp	Leu	Gly	Pro	Asn	Asp	Pro	Lys	Gln	Lys	Glu	Gln	Lys	Ala
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Ser	Arg	Asn	Lys	Gln	Glu	Phe	Glu	Gly	Thr	Phe	Met	Thr	Glu	Ala	Lys
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				245					250					255	
Phe	Ile	Ser	Val	Trp	Leu	Thr	Ala	Ala	Gly	Ile	Ile	His	Leu	Leu	Glu
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Trp	Thr	Cys	Val	Tyr	Phe	Leu	Ile	Val	Thr	Met	Ser	Thr	Val	Gly	Tyr
	290					295					300				
Gly	Asp	Val	Tyr	Cys	Glu	Thr	Val	Leu	Gly	Arg	Thr	Phe	Leu	Val	Phe
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Phe	Leu	Leu	Val	Gly	Leu	Ala	Val	Phe	Ala	Ser	Trp	Ile	Pro	Glu	Ile
				325					330					335	
Thr	Glu	Leu	Ala	Ala	Gln	Arg	Ser	Lys	Tyr	Gly	Gly	Thr	Tyr	Ser	Lys
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Thr Thr Tyr Phe Asn Gln Asn Ala Leu Thr Leu Ile Arg Ser Leu Ile
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Thr Gly Gly Ala Thr Pro Glu Leu Glu Leu Ile Leu Ala Glu Gly Ala
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Gly Leu Arg Gly Gly Tyr Ser Thr Val Glu Ser Leu Ser Asn Arg Asp
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Arg Cys Arg Val Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln
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Phe Gly Glu Cys Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys
 1075 1080 1085

Ser Tyr Gly Met Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser
 1090 1095 1100

Ser Ser Cys Asp Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro
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Asp Asp Phe Ser Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln
 1125 1130 1135

Phe Asp Pro Gly Leu Glu Tyr Lys Pro Pro Ala Val Arg Ala Pro Ala
 1140 1145 1150

Gly Gly Arg Gly Thr Asn Thr Gln Gly Ser Gly Val Gly Gly Gly Gly
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Ser Asn Lys Asp Asp Asn Ser Leu Ser Asn Arg Asp Arg Cys Arg Val
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Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln Phe Gly Glu Cys
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Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys Ser Tyr Gly Met
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Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser Ser Ser Cys Asp
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24

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<210> 34
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24

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<400> 53
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1

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